

1/14

LOCUS AT2 receptor C-terminal end 140 BP DS-DNA

ORGANISM Mouse

BASES 41 A 33 C 36 G 50 T

Nucleic acids 1 TGTGTTAATC CCTTCCTGTA TTGTTTGTG CGAAACCGCT
TCCAACAGAA CGTCCGCAGT GTGTTTAGAG TTCCCATAC
TTGGCTCCAA GGCAAGAGAG AGACTATGTC TTGCAGAAAA
121 GGCAGTTCTC TTAGAGAAAT GGACACCTTT GTGTCTTAAA

Translation into amino acids

CVNPELYCFV GNRFOQNVR VVRVPITWLO GKRETMSCRK
GSSLREMDTFVS-

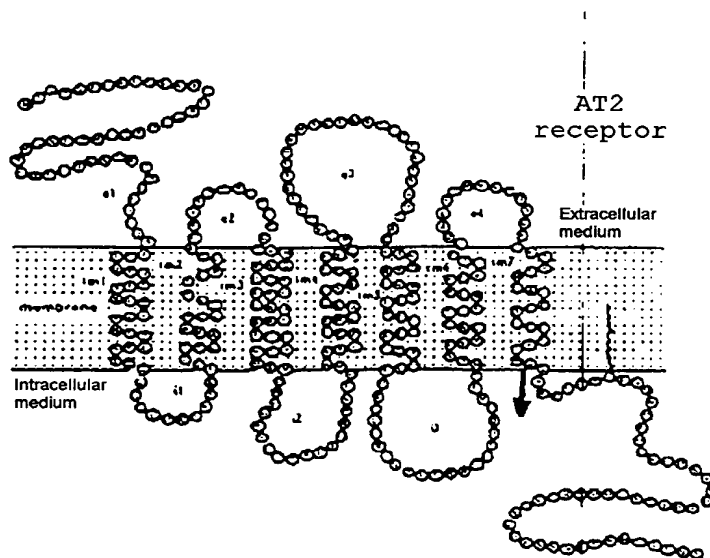


Figure 1

2/14

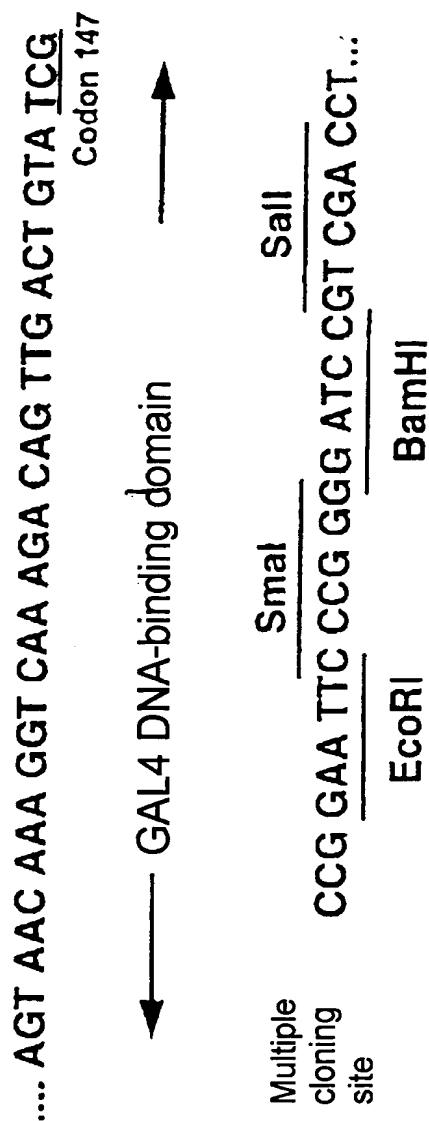


Figure 2

3/14

GCTACCCCCCCCCACGCCACCCCCCAATCTGGGTGGCATTAGCATGTAGCTTGTTCCTCTGGG 71
 TGTATCTCTTGGCCTGGAAGAACCCTGAGTTGCCAAGAGACACAGTATGTGATGGTCCCTGGAAAAGCTGCT 143
 TCCCCCTGCGAAGCTTCTCCCACTGGCTTGAAGAC M L L S b K F S L 9
 ATG CTG TCG TCT CCG AAA TTC TCG TTA 204
 S T I H V R L T A K G L L R N L R L 27
 TCC ACC ATC CAC GTC CGC CTA ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTC 258
 F S G L R K N T V I F H T V E K G R 45
 CCT TCG GGG CTC AGG AAA AAC ACT GTC ATT TTC CAC ACA GTT GAA AAG GGC AGG 312
 Q K N P R S L C E G T Q T A P D V L 53
 CAG AAG AAT CCC AGG AGC CTG TGC ATC CAG ACC CAG ACA GGT CCA GAT GTG CTG 356
 S S E R T L E L A Q Y K T K C E S Q 81
 TCC TCC GAG AGA ACG CTT GAG TTG GCC CAA TAC AAG ACA AAA TGT GAA AGC CAA 420
 S G F I L H L R Q L L S R G N N K F 99
 AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CTT TCC COT GGT AAC AAC AAG TTT 474
 E A L T V V I Q H L L S E R E E A L 117
 GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG CCG GAG GAA GCA CTG 523
 K Q H K T L S Q E L V S L R G E L V 135
 AAG CAA CAC AAA ACC CTC TCT CAA GAA CTT GTC AGC CTC CCG GGA GAG CTA GTT 582
 1 A A S S A C E K L E K A R A D L Q T 153
 GCT GCT TCA AGC GCC TGT GAG AAG CTA GAA AAG GGT AGG GCT GAC TTA CAG ACA 636
 A Y Q E F V Q K L N Q Q H Q T D R T 171
 GCG TAT CAA GAA TTT GTC CAG AAA CTA AAC CAG CAG CAT CAG ACA GAC CGG ACC 690
 E L E N R L K D L Y T A E C E K L Q 189
 GAA CTG GAG AAC CCG CTG AAG GAC TTA TAC ACC CCA GAG TGT GAG AAG CTT CAG 744
 S I Y I E E A E K Y K T Q L Q E Q F 207
 AGC ATT TAC ATT GAG GAG GCA GAA AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT 798
 D N L N A A H E T T K L E E E A S H 225
 2 GAC AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GGT AGC CAC 852
 S E K V E L L K K T Y E T S L S E E 243
 TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCT CTT TCA GAA ATC 906
 K K S H E H E K K S L E D L L N E K 261
 AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT CTG CTT AAT GAG AAG 960
 Q E S L E K Q E N D L H S E N D A L 279
 CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG AAG AGT GAA AAC GAT GGT TTA 1014
 3 N E R L K S E E Q K Q L S F E K A N 297
 AAC GAA AGG TTG AAA TCA GAG GAG CAA AAG CAA CTG TCA AGA GAG AAG GCG AAT 1068
 S K N P Q V M Y L E Q E L S S L K A 315
 TCC AAA AAC CCT CAG CTC ATG TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT 1132

Figure 3.1

4/14

4

V	L	E	I	K	N	E	K	L	H	Q	Q	D	M	K	L	M	K	333
GTG	TTA	GAG	ATC	AAG	AAT	GAG	AAG	CTG	CAC	CAG	CAG	GAC	ATG	AAG	CTA	ATG	AAG	1176
M	E	K	L	V	D	N	N	T	A	L	V	D	K	L	K	R	F	351
ATG	GAA	AAG	CTG	GTG	GAC	AAT	AAC	ACA	GCA	TTG	GTT	GAC	AAG	CTG	AAG	CSA	TTC	1230
Q	Q	E	N	E	E	L	K	A	R	M	D	K	H	M	A	I	S	369
CAG	CAG	GAA	AAC	GAG	GAG	TTA	AAA	GCT	CGC	ATG	GAC	AAA	GAC	ATG	GCA	ATT	TCA	1284
R	Q	L	S	T	E	Q	A	A	L	Q	E	S	L	E	K	E	S	387
AGG	CAA	CTT	TCC	ACC	GAG	CAG	GCC	GCG	CTG	CAA	GAG	TCC	CTT	GAG	AAG	GAG	TCA	1338
K	V	N	K	R	L	S	M	E	N	E	E	L	L	W	K	L	H	405
AAG	GTC	AAC	AAG	AGA	CTG	TCC	ATG	GAG	AAC	GAG	GAA	CTT	CTG	TGG	AAA	CTG	CAC	1392
N	G	D	L	C	S	P	K	R	S	P	T	S	S	A	I	P	F	423
AAC	GGA	GAC	CTG	TGC	AGC	CCC	AAG	AGA	TCC	CCC	ACC	TCC	TCC	GCC	ATC	CCT	TTC	1446
Q	S	P	R	N	S	G	S	F	S	S	P	S	I	S	P	R	*	440
CAG	TCC	CCC	AGG	AAT	TCT	GCT	TCC	TTC	TCC	AGC	CCC	AGC	ATC	TCA	CCC	AGA	TGA	1500
CGGCTTCTGAACGCAGGAGACTCTCTGAAGGCAGTGGGTGCGCTTCTGCAGGACTGACCCCTCTCATGGGA	1571																	
ACTCGAGTTGCTGCGTTAGCTCTCTGGAATATCCCCAGGATATCGGGAGAGCAGCCGCCAACCGTATCAGC	1642																	
TACGTACGAATAGAGAGCTCCAATACAAGACTTTTAACTTGGTCCAAAAGCCTCCTCCAAAACAGATTTC	1713																	
GGAACCTGAAGTGGACATAGTTGCACAAAGCACTTACGGAACGAGGGAACCTTCTTCTTTGCCTTCTTCAC	1784																	
CTAAGCATAGGCTTTTCAG	1803																	

Figure 32

5/14

cagctgtgacgtgggttcagagggcagctcttagacctgacggaggagattgtattcagagggaagagcaccatt 72
ctggcgaacatcttgaagctgaaacgggaagccgaacacacttgccagccctgggggacctctctctctctctct 144
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cgagcttaaaaagacagctatgtgacagctccatggaaaattgccccctctctgaaatctctgcccacctgtccga 288
agac atg ttg ttg tct ccc aaa ttc tcc tta tcc acc att cac ata cga ctg acc 360
H L L S P K F S L S T I H L R L T 17
GCC AAA GGA TGG CTT CGA AAC CTT CGA CTT CCT TCA GGG TTT AGG AGA AGC ACT 392
A K G L L R N L P S G F R R S T 35
GTT GTT TTC CAC ACA GTT GAA AAG AGC AGG CAA AAG AAT CCT CGA AGC TTA TGT 464
V V F H T V E K S R Q K N P R S L C 33
ATC CAG CCA CAG ACA GCT CCC GAT GCG CTG CCC CTT GAG AAA ACA CTT GAA TTG 536
I Q P Q T A P D A L P P E K T L E L 71
ACG CAA TAT AAA CTA AAA TGT GAA AAC CAA AGT GCA TTT ATC CTG CAG CTC AAG 608
T Q Y K T K C E N Q S G F I L Q L K 39
CAG CTT CTT GCC TGT GGT AAT ACC AAG TTT GAG GCA TTG ACA GTT GTG ATT CAG 680
Q L L A C G N T K F E A L T V V I Q 107
CAC CTG CTG TCT GAG GCG GAG GAA GCA CTG AAA CAA CAC AAA ACC CTA TCT CAA 752
H L L S E R E E A L K Q H K T L S Q 125
1 GAA CTT GTT AAC CTC CGG GGA GAG CTA GTC ACT GCT TCA ACC ACC TGT GAG AAA 824
E L V N L R G E L V T A S T T C E K 143
TTA GAA AAA GCC AGG AAT GAG TTA CAA ACA GTG TAT GAA GCA TTC GTC CAG CAG 896
L E X A R N E L Q T V Y E A F V Q Q 161
CAC CAG GCT GAA AAA ACA GAA CGA GAG AAT CGG CTT AAA GAG TTT TAC ACC AGG 968
H Q A E K T E R E N R L K E F Y T R 179
GAG TAT GAA AAG CTT CGG GAC ACT TAC ATT GAA GAA GCA GAG AAG TAC AAA ATG 1040
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2 ATT GAA GCT AGC CAC TCA GAG AAA CTT GAA TTG CTA AAG AAG GCC TAT GAA GCC 1184
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TCC CTT TCA GAA ATT AAG AAA GGC CAT GAA ATA GAA AAG AAA TCG CTT GAA GAT 1256
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3 GAA AAT GAT GCT TTA AAT GAA AAA TTG AAA TCA GAA GAA CAA AAA AGA AGA GCA 1400
E N D A L N E K L K S E E Q K R R A 287
AGA GAA AAA GCA AAT TTG AAA AAT CCT CAG ATC ATC TAT CTA GAA CAG GAG TTA 1472
R E K A N L K N P Q I H Y L E Q E L 305

Figure 41

6/14

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GAA AGC CTG AAA GCT GTC TTA GAG ATC AAG AAT GAG AAA CTG CAT CAA CAG GAC 1361
E S L K A V L E I K N E K L H Q G D 323

ATC AAG TTA ATG AAA ATG GAC AAA CTG GTG GAC AAC AAC ACA GCA TTG GTT GAC 1315
I K L N K H E K L V D N N T A L V D 341

AAA TTG AAG CGT TTC CAG CAG GAG AAT GAA GAA TTG AAA GTT CCG ATG GAC AAG 1359
K L K R F Q Q E N E E L X A R M D K 359

CAC ATG GCA ATC TCA AGG CAG CTT TCC ACS GAG CAG GCT GTT CTG CAA GAG TCG 1423
H M A I S R Q L S T E Q A V L Q E S 377

CTG GAG AAG GAG TCG AAA GTC AAC AAG CGA CTC TCT ATG GAA AAC CAG GAG CTT 1477
L E K E S K V N K R L S H E N E E L 395

CTG TGG AAA CTG CAC AAT GGG GAC CTG TGT AGC CCC AAG AGA TCC CCC ACA TCC 1531
L W K L H N G D L C S P K Z S P T S 413

TCC GCC ATC CCT TTG CAG TCA CCA AGG AAT TCG GGT TCC TTC CCT AGC CCC AGC 1585
S A I P L Q S P R N S G S T P S P S 431

ATT TCA CCC AGA TGA cagctccccaaagctccacagactctctgaagcatctctgacgaggtccgc 1651
I S P R 436

aggactcagccccaaagaggaacgtgggcacaaagaggtatctcagcacacgtctgacacccctaggtcactcg 1723

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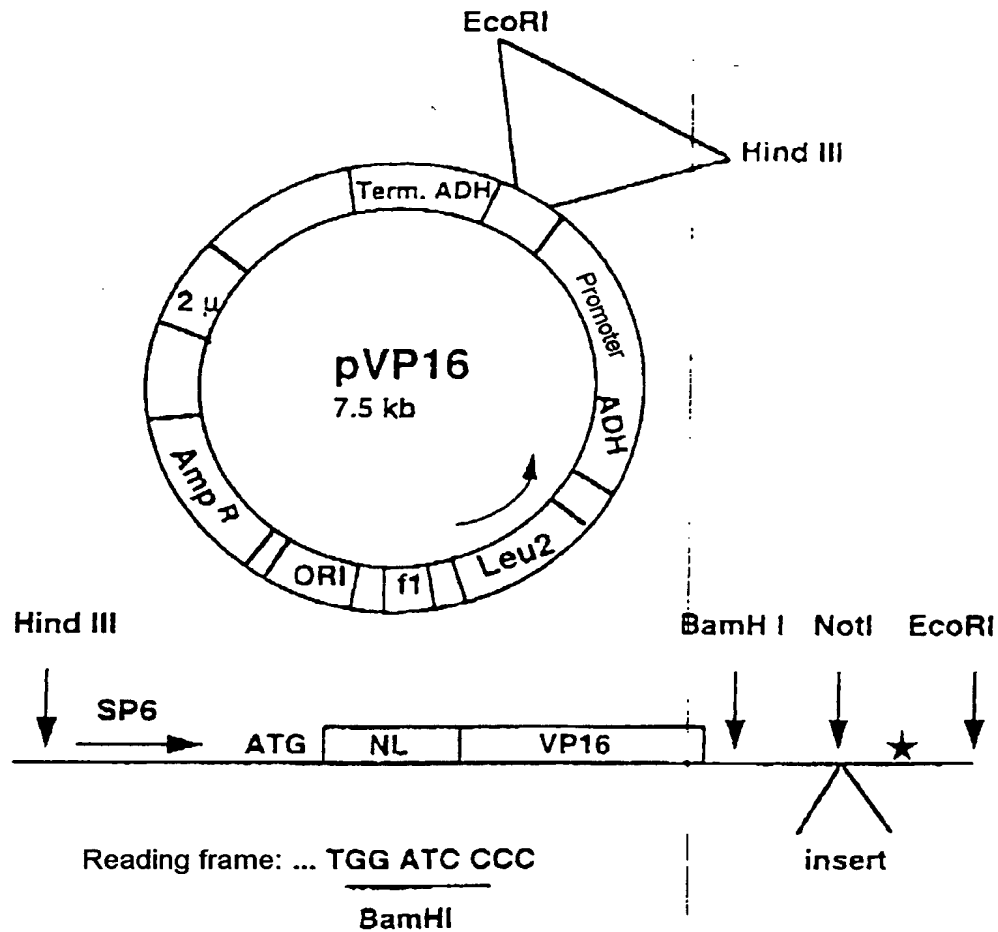
Figure 4.2

7/14

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cccaggatgcttagaggtgaactatccgggtcattcacatgtacactacataagcagctgatactcatgttgc 3215
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ctgtagaattgcadaatctctgctacgtctaaaaaatatgaaagtgttagacaaactgttgtctgtctcagctctgtagt 3667
gatgggaagtgtatctctacccctgaccaaataaaataatgtctggaaatcttcaaaaataaaaaaaaaaaaaaaaaa 3739
aaa 3742
```

Figure 4.3

8/14



★ Stop codons in three frames

pVP16 was constructed by Stan Hollenberg

Figure 5

9/14

6 histidines

98... ATG CGG GGT TCT CAT CAT CAT CAT CAT GGT ATG
134 GCT AGC ATG ACT GGT GGA CAG CAA ATG GGT CGG GAT
170 CTG TAC GAC GAT GAC GAT AAG GAT CGA TGG GGA TCC
206 GAG CTC GAG ATC TGC AGC TGG TAC CAT GGA ATT CGA
242 AGC TTG ATC CGG CTG CTA ACA AAG CCC GAA AGG AAG
278 CTG AGT TGG CTG CCA CCG CTG AGC AAT AAC TAG...

BamH I

Figure 6

10/14

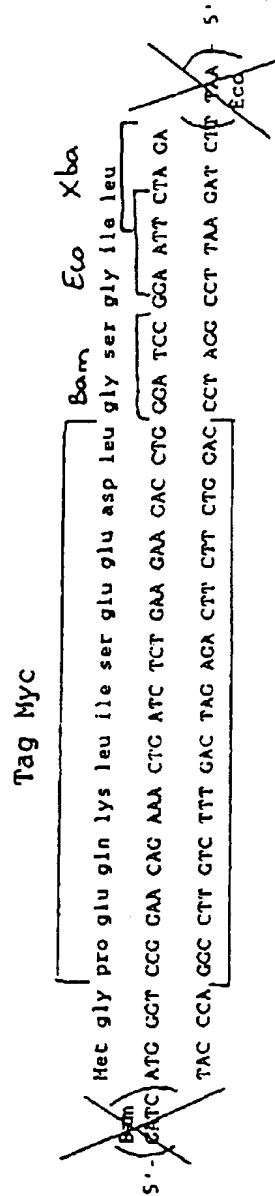
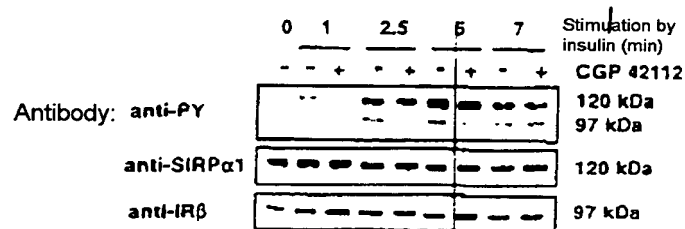
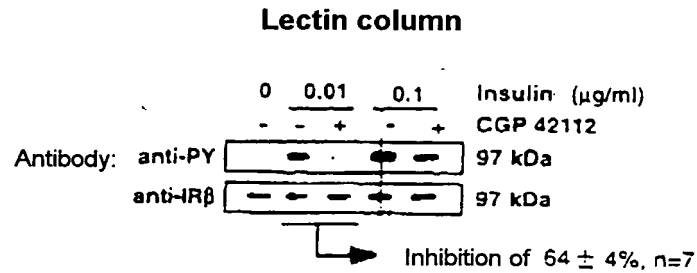


Figure 7

14 / 14

CHO-hAT2



CHO-hAT2 et CHO-hAT2-ATIP

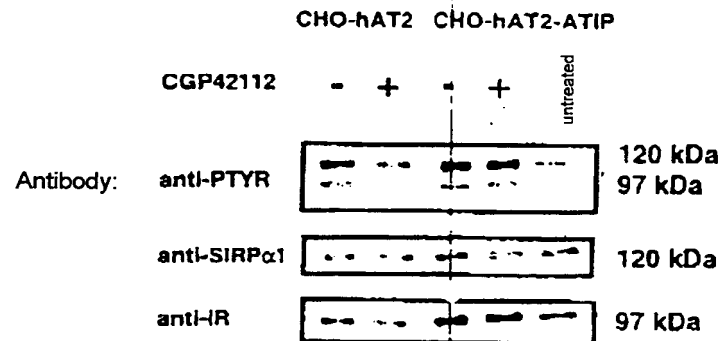
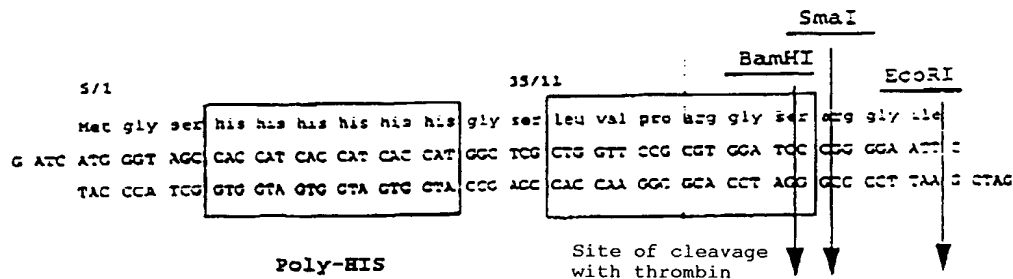


Figure 11

11/14



pBacPAK1-poly HIS -> Graphic Map

DNA sequence 5526 b.p. AACCGCTCCGCTTATTAAATCCAG circular

PolyHIS insertion into pBackpack in BamHI(CACCAT) 1270-1287

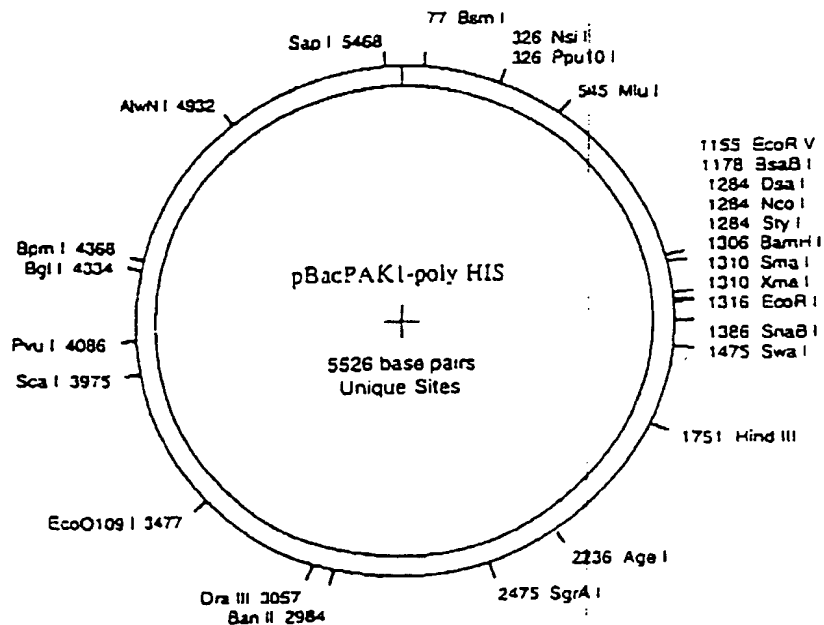


Figure 8

12/14

Tissues:

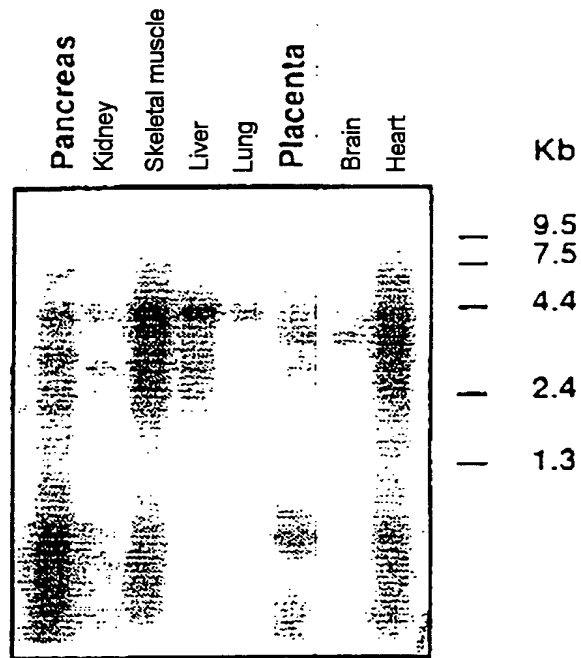


Figure 9

Figure 10